

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Pelleymounter, Mary Ann  
 Hecht, Randy I  
 Mann, Michael B

(ii) TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.  
 (B) STREET: 1840 Dehavilland Drive  
 (C) CITY: Thousand Oaks  
 (D) STATE: California  
 (E) COUNTRY: U.S.A.  
 (F) ZIP: 91230-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/474,833  
 (B) FILING DATE: 07-JUN-1995  
 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pessin, Karol M.  
 (C) REFERENCE/DOCKET NUMBER: A-345

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTAGATTTG AGTTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAGT	60
TCAGGACGAC ACCAAAACCT TAATTAACAC GATCGTTACG CGTATCAACG ACATCAGTCA	120
CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA	180
CCCGATCCTA AGCTTGTCCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC	240
CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACC TTCGCGACCT	300
GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA	360

ACCGGAATCC	CTGGACGGGG	TCCTGGAAGC	ATCCCTGTAC	AGCACCGAAG	TTGTTGCTCT	420
GTCCCGTCTG	CAGGGTTCCC	TTCAGGACAT	CCTTCAGCAG	CTGGACGTTT	CTCCGGAATG	480
TTAATGGATC	C					491

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 491 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGATCTAAC	TCAAAATTGA	AAATCTTCCT	CCTTATTGTA	TACCATGGCT	AGGTCTTTCA	60
AGTCCTGCTG	TGGTTTTGGA	ATTAATTTCG	CTAGCAATGC	GCATAGTTGC	TGTAGTCAGT	120
GTGGGTCAGC	CAGAGGCGAT	TTGTCGCACA	ATGGCCAGAC	CTGAAGTAGG	GCCCAGACGT	180
GGGCTAGGAT	TCGAACAGGT	TTTACCTGGT	CTGGGACCGA	CATATGGTCG	TCCACAATTG	240
GAGGGACGGC	AGGGTCTTGC	AAGAAGTCTA	GCGATTGCTG	GAGCTCTTGG	AAGCGCTGGA	300
CGACGTGGAC	GACCGTAAGA	GGTTTAGGAC	GAGGGACGGC	GTCTGGAGTC	CAGAAGTCTT	360
TGGCCTTAGG	GACCTGCC	AGGACCTCG	TAGGGACATG	TCGTGGCTTC	AACAACGAGA	420
CAGGGCAGAC	GTCCCCAAGGG	AAGTCCTGTA	GGAAGTCGTC	GACCTGCAA	GAGGCCTTAC	480
AATTACCTAG	G					491

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 147 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	Thr	Leu	Ile	Lys
1				5				10			15				
Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	Gln	Ser	Val	Ser
	20				25						30				
Ala	Lys	Gln	Arg	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	Gly	Leu	His	Pro
	35				40						45				
Ile	Leu	Ser	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	Val	Tyr	Gln	Gln

50	55	60													
Val	Leu	Thr	Ser	Leu	Pro	Ser	Gln	Asn	Val	Leu	Gln	Ile	Ala	Asn	Asp
65					70				75					80	
Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Leu	Leu	Ala	Phe	Ser	Lys	Ser
				85				90					95		
Cys	Ser	Leu	Pro	Gln	Thr	Ser	Gly	Leu	Gln	Lys	Pro	Glu	Ser	Leu	Asp
				100				105				110			
Gly	Val	Leu	Glu	Ala	Ser	Leu	Tyr	Ser	Thr	Glu	Val	Val	Ala	Leu	Ser
				115				120				125			
Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Ile	Leu	Gln	Gln	Leu	Asp	Val	Ser
				130			135				140				
Pro	Glu	Cys													
		145													

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 454 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATATGGTAC	CGATCCAGAA	AGTCAGGAC	GACACCAAAA	CCTTAATTAA	AACGATCGTT	60
ACGGGTATCA	ACGACATCAG	TCACACCCAG	TCGGTGAGCT	CTAACACAGCG	TGTTACAGGC	120
CTGGACTTCA	TCCCCGGTCT	GCACCCGATC	CTGACCTTGT	CCAAATGGA	CCAGACCCCTG	180
GCTGTATACC	AGCAGATCTT	AACCTCCATG	CCGTCCCGTA	ACGTTCTTCA	GATCTCTAAC	240
GACCTCGAGA	ACCTTCGCGA	CCTGCTGCAC	GTGCTGGCAT	TCTCCAAATC	CTGCCACCTG	300
CCATGGGCTT	CAGGTCTTGA	GACTCTGGAC	TCTCTGGCG	GGGTCTGGGA	AGCATCCGGT	360
TACAGCACCG	AAGTTGTTGC	TCTGTCCCGT	CTGCAGGGTT	CCCTTCAGGA	CATGCTTTGG	420
CAGCTGGACC	TGTCTCCGGG	TTGTTAATGG	ATCC			454

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 454 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTATACCATG	GCTAGGTCTT	TCAAGTCCTG	CTGTGGTTTT	GGAATTAATT	TTGCTAGCAA	60
TGCGCATAGT	TGCTGTAGTC	AGTGTGGTC	AGCCACTCGA	GATTTGTCGC	ACAATGTCCG	120
GACCTGAAGT	AGGGCCCAGA	CGTGGGCTAG	GACTGGAACA	GGTTTTACCT	GGTCTGGGAC	180
CGACATATGG	TCGTCTAGAA	TTGGAGGTAC	GGCAGGGCAT	TGCAAGAAGT	CTAGAGATTG	240
CTGGAGCTCT	TGGAAGCGCT	GGACGACGTG	CACGACCGTA	AGAGGTTTAG	GACGGTGGAC	300
GGTACCCGAA	GTCCAGAACT	CTGAGACCTG	AGAGACCCGC	CCCAGGACCT	TCGTAGGCCA	360
ATGTCGTGGC	TTCAACAACG	AGACAGGGCA	GACGTCCCAA	GGGAAGTCCT	GTACGAAACC	420
GTCGACCTGG	ACAGAGGCC	AAACAATTACC	TAGG			454

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys	1	5	10	15
Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser	20	25	30	
Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro	35	40	45	
Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln	50	55	60	
Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp	65	70	75	80
Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser	85	90	95	
Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly	100	105	110	
Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser	115	120	125	
Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser	130	135	140	
Pro Gly Cys	145			